

## SEQUENCE LISTING

<110> K. Sampath et al.

<120> METHODS FOR MAINTAINING OR RESTORING TISSUE-APPROPRIATE PHENOTYPE OF  
SOFT TISSUE CELLS

<130> CIBT-P01-520

<140> 09/581,770

<141> 2000-12-29

<150> PCT/US98/26788

<151> 1998-12-16

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 1067

<212> DNA

<213> Mus musculus

<400> 1

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tccctatagg aaattgcacc agtagtcaac tggattttta aaaggcaaag cttgaggatt      180
tttttttccc ttgaaatga atgtagcaaa cttatgtaag cacggaatag gattattagt      240
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taattagtgc ttcttgcccc tgagaggagg agcttcgggt caggggaact tcatgcaata      960
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1067

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Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
   5                               10                               15

ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac      153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
  20                               25                               30                               35

gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg      201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
                               40                               45                               50

cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc      249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
   55                               60                               65

ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg      297
Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
   70                               75                               80

ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc      345
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
   85                               90                               95

ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc      393
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
  100                               105                               110                               115

ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac      441
Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
   120                               125                               130

atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc      489
Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
   135                               140                               145

cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc      537
His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
   150                               155                               160

cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac      585
Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
   165                               170                               175

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ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro 245 250 255	825
aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro 260 265 270 275	873
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gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370	1161
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ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390 395 400	1257
atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415	1305

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 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His  
 420 425 430

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Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala  
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 20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser  
 35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu  
 50 55 60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro  
 65 70 75 80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly  
 85 90 95

Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser  
 100 105 110

Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr  
 115 120 125

Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys  
 130 135 140

Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu  
 145 150 155 160

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile  
 165 170 175

Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile  
 180 185 190

Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu  
 195 200 205

Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu  
 210 215 220

Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg  
 225 230 235 240

His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser  
 245 250 255

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn  
 260 265 270

Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe  
 275 280 285

Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser  
 290 295 300

Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu  
 305 310 315 320

Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr  
 325 330 335

Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu  
 340 345 350

Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn  
 355 360 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His  
 370 375 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln  
 385 390 395 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile  
 405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His  
 420 425 430